GEPHE SUMMARY

Gephebase Gene
Zmr1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Zmr1^#gephebase-summary-title)

GepheID
GP00001715

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

Trait #1

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait
Xenobiotic resistance (fungicide) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (fungicide)^#gephebase-summary-title)

Trait State in Taxon A
high melanin levels - lower growth rate in absence of funcicide - higher growth rate in presence of fungicide

Trait State in Taxon B
low melanin levels - higher growth rate in absence of funcicide

Trait #2

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait
Melanin content (https://www.gephebase.org/search-criteria?/and+Trait=^Melanin content^#gephebase-summary-title)

Trait State in Taxon A
high melanin levels - lower growth rate in absence of funcicide - higher growth rate in presence of fungicide

Trait State in Taxon B
low melanin levels - higher growth rate in absence of funcicide

Ancestral State
Data not curated

Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name
Zymoseptoria tritici (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zymoseptoria tritici^#gephebase-summary-title)

Common Name
-

Synonyms
Zymoseptoria tritici (Desm.) Quaedvlieg & Crous 2011; CBS 115943; CBS:115943; IPO 323; IPO:323

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; dothideomyceta; Dothideomycetes; Dothideomycetidae; Capnodiales; Mycosphaerellaceae; Zymoseptoria

Parent
Zymoseptoria () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047167)

NCBI Taxonomy ID
1047171 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047171)

is Taxon A an Infraspecies?
Yes

Taxon A Description
strain 3D7

Taxon B

Latin Name
Zymoseptoria tritici (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Zymoseptoria tritici^#gephebase-summary-title)

Common Name
-

Synonyms
Zymoseptoria tritici (Desm.) Quaedvlieg & Crous 2011; CBS 115943; CBS:115943; IPO 323; IPO:323

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; dothideomyceta; Dothideomycetes; Dothideomycetidae; Capnodiales; Mycosphaerellaceae; Zymoseptoria

Parent
Zymoseptoria () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047167)

NCBI Taxonomy ID
1047171 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047171)

is Taxon B an Infraspecies?
Yes

Taxon B Description
strain 3D1

GENOTYPIC CHANGE

Generic Gene Name

CMR1

Synonyms

-

String

-

Sequence Similarities

-

UniProtKB Cochliobolus heterostrophus

Q06F33 (http://www.uniprot.org/uniprot/Q06F33)

GenebankID or UniProtKB

()

GO - Molecular Function

GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)

GO - Biological Process

GO:0006351 : transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006351)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Mutation #1

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title)

Insertion Size

10-100 kb

Molecular Details of the Mutation

insertion of a transposable element island (13 TE interspersed by simple repeats) of approximately 30 kb, located 1862 bp upstream of Zmr1 start codon - analysis of knock out lines of the TE island insertion

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

Main Reference

Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. (2018) (https://pubmed.ncbi.nlm.nih.gov/30012138)

Authors

Krishnan P; Meile L; Plissonneau C; Ma X; Hartmann FE; Croll D; McDonald BA; SÃ¡nchez-Vallet A

Abstract

Fungal plant pathogens pose major threats to crop yield and sustainable food production if they are highly adapted to their host and the local environment. Variation in gene expression contributes to phenotypic diversity within fungal species and affects adaptation. However, very few cases of adaptive regulatory changes have been reported in fungi and the underlying mechanisms remain largely unexplored. Fungal pathogen genomes are highly plastic and harbor numerous insertions of transposable elements, which can potentially contribute to gene expression regulation. In this work, we elucidated how transposable elements contribute to variation in melanin accumulation, a quantitative trait in fungi that affects survival under stressful conditions.

We demonstrated that differential transcriptional regulation of the gene encoding the transcription factor Zmr1, which controls expression of the genes in the melanin biosynthetic gene cluster, is responsible for variation in melanin accumulation in the fungal plant pathogen Zymoseptoria tritici. We show that differences in melanin levels between two strains of Z. tritici are due to two levels of transcriptional regulation: (1) variation in the promoter sequence of Zmr1 and (2) an insertion of transposable elements upstream of the Zmr1 promoter. Remarkably, independent insertions of transposable elements upstream of Zmr1 occurred in 9% of Z. tritici strains from around the world and negatively regulated Zmr1 expression, contributing to variation in melanin accumulation.

Our studies identified two levels of transcriptional control that regulate the synthesis of melanin. We propose that these regulatory mechanisms evolved to balance the fitness costs associated with melanin production against its positive contribution to survival in stressful environments.

Additional References

Mutation #2

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)

Molecular Details of the Mutation

several candidate SNP - tests using reporter transgenes

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@TE ; check for UniProtKB and orthology with Cmr1